NUCLEIC ACID LIGANDS TO INTEGRINS

Cross Reference to Related Applications

This application is a divisional of U.S. Patent Application Serial No. 09/364,543, filed July 29, 1999, entitled "Nucleic Acid Ligands to Integrins," which is a continuation in part of U.S. Patent Application Serial No. 09/606,477, filed June 29, 2000, which is a continuation of U.S. Patent Application Serial No. 08/956,699, filed October 23, 1997, now U. S. Patent No. 6,083,696, which is a continuation of U.S. Patent Application Serial No. 08/234,997, filed April 28, 1994, now U.S. Patent No. 5,683,867, all entitled "Systematic Evolution of Ligands by Exponential Enrichment: Blended SELEX." U.S. Patent No. 5,683,867 is a continuation in part of U.S. Patent Application Serial No. 07/714,131, filed June 10, 1991, entitled "Nucleic Acid Ligands," now U.S. Patent No. 5,475,096.

Field of the Invention

This invention is directed towards nucleic acid ligands of integrins isolated using the SELEX process. SELEX is an acronym for Systematic Evolution of Ligands by EXponential Enrichment. This invention relates to integrin proteins, and methods and compositions for treating and diagnosing diseases involving integrins.

Background of the Invention

The integrins are a class of heterodimeric integral membrane proteins, one or more of which are expressed by most cell types (Hynes (1992) Cell 69:11-25). Some 16 homologous alpha subunits and 8 homologous beta subunits associate in various combinations to yield an extensive family of receptors. Each integrin heterodimer has a large extracellular domain that mediates binding to specific ligands. These ligands may include plasma proteins, proteins expressed on the surface of adjacent cells, or components of the extracellular matrix. Several of the integrins show affinity for more than one ligand and many have overlapping specificities (Hynes (1992) Cell 69:11-25). Both the α and β subunits contribute to a small intracellular domain that contacts

components of the actin cytoskeleton, thus forming a physical link between proteins outside and inside the cell. Integrins play an important role in cellular adhesion and migration, and these properties are controlled by the cell, in part, by modulation of integrin affinity for its ligands (so-called "inside-out" signaling). Conversely, the presence or absence of integrin ligation provides specific information about the cellular microenvironment, and in many instances integrins serve as a conduit for signal transduction. Ligand binding by an integrin may promote its incorporation into focal adhesions, the assembly of cytoskeletal and intracellular signaling molecules into supra-molecular complexes, and the initiation of a cascade of downstream signaling events including protein phosphorylation, calcium release, and an increase in intracellular pH (reviewed by Schwartz *et al.* (1995) Ann. Rev. Cell Dev. Biol. 11:549-99). Such "outside-in" signaling ties into pathways controlling cell proliferation, migration and apoptosis (Stromblad *et al.* (1996) J. Clin. Invest. 98:426-33; Eliceiri *et al.* (1998) J. Cell. Biol. 140:1255-63). Integrins have been shown to play a role in such diverse physiological settings as embryonic development, wound healing, angiogenesis, clot formation, leukocyte extravasation, bone resorption and tumor metastasis.

The β_3-containing integrins are among the best studied of the receptor superfamily. The β_3 subunit forms heterodimers with either α_v ($\alpha_v\beta_3$) or α_{IIb} ($\alpha_{IIb}\beta_3$). While these integrins show substantial overlap in ligand specificity, they play very different roles in normal physiology and in disease.

$\alpha_v\beta_3$ is expressed by activated endothelial cells, smooth muscle cells, osteoclasts, and, at a very low level, by platelets. It is also expressed by a variety of tumor cell types. The integrin binds to a number of plasma proteins or proteins of the extracellular matrix, many of which are associated with sites of inflammation or wound healing (Albelda (1991) Am. J. Resp. Cell Mol. Biol. 4:195-203). These include vitronectin, fibronectin, osteopontin, von Willebrand factor, thrombospondin, fibrinogen, and denatured collagen Type I (Hynes (1992) Cell 69:11-25). Each of these proteins share a common sequence motif, arginine-glycine-aspartic acid (RGD), that forms the core of the integrin binding site.

$\alpha_v\beta_3$ has been most intensely studied in the context of new blood vessel formation (angiogenesis) where it mediates the adhesion and migration of endothelial cells through

the extracellular matrix. Angiogenesis in adults is normally associated with the cyclical development of the corpus luteum and endometrium and with the formation of granulation tissue during wound repair. In the latter case, microvascular endothelial cells form vascular sprouts that penetrate into the temporary matrix within a wound. These cells transiently express $\alpha_v\beta_3$ and inhibition of the ligand binding function of the integrin temporarily inhibits the formation of granulation tissue (Clark *et al.* (1996) Am. J. Pathol. 148:1407-21). In cytokine-stimulated or unstimulated angiogenesis on the chick chorioallantoic membrane, blockade of $\alpha_v\beta_3$ with a heterodimer-specific antibody prevents new vessel formation without affecting the pre-existing vasculature (Brooks *et al.* (1994) Science 264:569-71). Furthermore, the loss of adhesive contacts by endothelial cells activated for angiogenesis induces a phenotype characteristic of apoptotic cells (Brooks *et al.* (1994) Cell 79:1157-64); that is, ligand binding by $\alpha_v\beta_3$ appears to transmit a survival signal to the cell. Thus, adhesion and/or signaling mediated by $\alpha_v\beta_3$ is essential for the formation of new blood vessels.

Solid tumors are unable to grow to significant size without an independent blood supply. It is currently hypothesized that the acquisition of an angiogenic phenotype is one of the limiting steps in the growth of primary tumors and of tumors at secondary sites (Folkman (1995) Nat. Med. 1:27-31). In addition, while the vasculature that penetrates a tumor mass provides a source of oxygen and nutrients, it also serves as a conduit for metastatic cells to leave the primary tumor and migrate throughout the body. Thus, inhibition of angiogenesis may limit both the growth and metastasis of cancerous lesions. In experimental settings of tumor-induced angiogenesis, inhibition of ligand-binding by endothelial $\alpha_v\beta_3$ prevented the formation of new blood vessels (Brooks *et al.* (1994) Cell 79:1157-64; Brooks *et al.* (1995) J. Clin. Invest. 96:1815-22), and inhibitors of $\alpha_v\beta_3$ were shown to reduce the growth of experimental tumors *in vivo* (Brooks *et al.* (1995) J. Clin. Invest. 96:1815-22; Carron *et al.* (1998) Canc. Res. 58:1930-5).

$\alpha_v\beta_3$ is not only expressed by the microvasculature within tumors, but in some cases, is also found on the surface of tumor cells themselves. In particular, expression of $\alpha_v\beta_3$ integrin has been detected in tissue sections from tumors of melanocytic and astroglial origin (Albelda *et al.* (1990) Canc. Res. 50:6757-64; Gladson and Cheresh (1991) J. Clin. Invest. 88:1924-32), and the level of integrin expression has been

correlated with the stage or metastatic potential of the tumor (Albelda *et al.* (1990) Canc. Res. 50:6757-64; Gladson *et al.* (1996) Am. J. Pathol. 148:1423-34; Hieken *et al.* (1996) J. Surg. Res. 63:169-73). Furthermore, melanoma cells grown *in vitro* in a three-dimensional matrix of denatured collagen undergo apoptosis upon $\alpha_v\beta_3$ blockade.

Data such as these have driven an interest in inhibitors of $\alpha_v\beta_3$ for the treatment of cancer. At present, two such inhibitors are in or near clinical trial: Vitaxin is a chimeric Fab fragment derived from the $\alpha_v\beta_3$-specific monoclonal antibody, LM609 (Wu *et al.* (1998) Proc. Nat. Acad. Sci. 95:6037-42). A phase I trial in late-stage cancer patients has been completed and no significant treatment-associated toxicities were observed (Gutheil *et al.* (1998) Am. Soc. Clin. Onc.). EMD121974 is a cyclic pentapeptide inhibitor of $\alpha_v\beta_3$. A Phase I study of this compound in Kaposi's sarcoma, brain tumors and solid tumors is scheduled to begin in 1999.

Angiogenesis (and $\alpha_v\beta_3$) are implicated in the pathology of several other diseases, including psoriasis (Creamer *et al.* (1995) Am. J. Pathol. 147:1661-7), rheumatoid arthritis (Walsh *et al.* (1998) Am. J. Pathol. 152:691-702; Storgard *et al.* (1999) J. Clin. Invest. 103:47-54), endometriosis (Healy *et al.* (1998) Hum. Reprod. Update 4:736-40), and several proliferative diseases of the eye (Casaroli Marano *et al.* (1995) Exp. Eye Res. 60:5-17; Friedlander *et al.* (1996) Proc. Nat. Acad. Sci. 93:9764-9; Hammes *et al.* (1996) Nat. Med. 2:529-33). Inhibition of integrin ligand binding in each of these contexts may provide significant therapeutic benefit.

Atheromatous plaque and restenosis following angioplasty are pathologies characterized by thickening of the intima, the innermost layer of the arterial wall. The proliferation and/or migration of smooth muscle cells into the neointima with concomitant deposition of fibrous extracellular proteins contributes to vessel wall thickening and subsequent vessel occlusion. Platelets may also contribute to the development of restenotic lesions through adhesion to endothelial cells and the release of growth factors and cytokines that stimulate the underlying smooth muscle cell layer (Le Breton *et al.* (1996) J. Am. Coll. Cardiol. 28:1643-51). $\alpha_v\beta_3$ integrin is expressed on arterial smooth muscle cells (Hoshiga *et al.* (1995) Circ. Res. 77:1129-35) and mediates their migration on vitronectin and osteopontin (Brown *et al.* (1994) Cardiovasc. Res. 28:1815-20; Jones *et al.* (1996) Proc. Nat. Acad. Sci. 93:2482-7; Liaw *et al.* (1995) J.

Clin. Invest. 95:713-24; Panda *et al.* (1997) Proc. Nat. Acad. Sci. 94:9308-13), both matrix proteins that are associated with atheroschlerotic tissues *in vivo* (Brown *et al.* (1994) Cardiovasc. Res. 28:1815-20; Giachelli *et al.* (1995) Ann. N. Y. Acad. Sci. 760:109-26; Panda *et al.* (1997) Proc. Nat. Acad. Sci. 94:9308-13). In addition, $\alpha_v\beta_3$ expression on endothelial cells, and to a much lesser extent on platelets, is responsible for at least part of the adhesive interaction between these cell types (Le Breton *et al.* (1996) J. Am. Coll. Cardiol. 28:1643-51; Gawaz *et al.* (1997) Circulation 96:1809-18). $\alpha_v\beta_3$ blockade with RGD-containing peptides or a monoclonal antibody was found to limit neointimal hyperplasia in several animal models of restenosis following arterial injury (Choi *et al.* (1994) J. Vasc. Surg. 19:125-34; Srivatsa *et al.* (1997) Cardiovasc. Res. 36:408-28; Slepian *et al.* (1998) Circulation 97:1818-27; Coleman *et al.* (1999) Circ. Res. 84:1268-76). Furthermore, treatment of patients undergoing percutaneous coronary intervention with an anti-β3 antibody (Reopro/abciximab/c7E3), which blocks both the platelet fibrinogen receptor, $\alpha_{IIb}\beta_3$, and $\alpha_v\beta_3$, provided long term reduction in the rates of death or myocardial infarction and in the rate of reocclusion of the artery (Lefkovits *et al.* (1996) Am. J. Cardiol. 77:1045-51), an effect that may be mediated through inhibition of $\alpha_v\beta_3$ ligation. The observation that $\alpha_v\beta_3$ is expressed by microvascular smooth muscle cells after experimentally-induced focal cerebral ischemia (Okada *et al.* (1996) Am. J. Pathol. 149:37-44) suggests that this integrin may also play some role in the development of ischemia/reperfusion injury in stroke.

Finally, $\alpha_v\beta_3$ mediates the attachment of osteoclasts to matrix proteins, particularly osteopontin, on the surface of bone. Osteoclasts are responsible for the resorption of bone in normal physiology as well as in pathological conditions such as osteoporosis. A monoclonal antibody specific for $\alpha_v\beta_3$ inhibited the binding and resorption of bone particles by osteoclasts *in vitro* (Ross *et al.* (1993) J. Biol. Chem. 268:9901-7). Furthermore, an RGD-containing protein, echistatin, was shown to block parathyroid-stimulated bone resorption in an animal model, as monitored by serum calcium levels (Fisher *et al.* (1993) Endocrin. 132:1411-3). Inhibitors of $\alpha_v\beta_3$ integrin are thus considered of potential utility in treating debilitating bone loss such as occurs in osteoporosis.

$\alpha_{IIb}\beta_3$ (also referred to as GPIIbIIIa) is the major integrin on the surface of platelets where it mediates the adhesion of activated platelets to the plasma protein fibrinogen (Nachman and Leung (1982) J. Clin. Invest. 69:263-9; Shattil *et al.* (1985) J. Biol. Chem. 260:11107-14). During clot formation, fibrinogen dimers cross-link platelets to one another through the integrin receptor. $\alpha_{IIb}\beta_3$ also binds to several other plasma and cell matrix proteins, including von Willebrand factor, vitronectin, and fibronectin (Faull and Ginsberg (1996) J. Am. Soc. Nephrol. 7:1091-7).

Clot formation is a tightly regulated process that balances the need for rapid response to vascular injury with the risk of aberrant occlusion of critical vessels. The $\alpha_{IIb}\beta_3$ heterodimer is constitutively expressed on the surface of resting platelets at approximately 80,000 copies per cell (Wagner *et al.* (1996) Blood 88:907-14); however, the affinity of the integrin for fibrinogen is very low on these cells. Activation of platelets by ADP, epinephrine, collagen or thrombin leads to a dramatic enhancement in integrin ligand binding activity (Bennett and Vilaire (1979) J. Clin. Invest. 64:1393-401; Marguerie *et al.* (1979) J. Biol. Chem. 254:5357-63), probably accomplished through a conformational change in the receptor (Shattil *et al.* (1985) J. Biol. Chem. 260:11107-14; O'Toole *et al.* (1990) Cell Reg. 1:883-93; Du *et al.* (1993) J. Biol. Chem. 268:23087-92). In this prototypic example of "inside-out" control of integrin function, cross-linking of platelets through the $\alpha_{IIb}\beta_3$-fibrinogen interaction is confined to local sites of platelet activation.

Inhibitors of $\alpha_{IIb}\beta_3$ ligand binding have been primarily explored in the context of cardiovascular disease (Chong (1998) Am. J. Health Syst. Pharm. 55:2363-86; Topol *et al.* (1999) Lancet 353:227-31), but may have application in any of a number of indications where thrombus formation is suspected or is likely. Three $\alpha_{IIb}\beta_3$ inhibitors have been approved for use in patients experiencing acute coronary syndrome and/or in patients who are undergoing percutaneous coronary intervention. Reopro (Centocor/Eli Lilly) is a humanized murine monoclonal antibody Fab fragment with specificity for the β_3 chain of $\alpha_{IIb}\beta_3$. Integrilin (COR Therapeutics) is a cyclic heptapeptide based on the integrin binding site of barbourin, an $\alpha_{IIb}\beta_3$ inhibitory protein derived from snake venom. Aggrastat (Merck & Co.) is a non-peptide small molecule antagonist of the integrin. Unlike the small molecule inhibitors, Reopro cross-reacts with $\alpha_v\beta_3$, a fact which may

account for the greater reduction in long-term rates of death and non-fatal myocardial infarction associated with its use (see above). A significant effort is underway to identify new inhibitors of the platelet integrin with characteristics not found in the cohort of approved drugs. Specifically, compounds with specificity for the active, ligand-binding conformation of $\alpha_{IIb}\beta_3$ may reduce the risk of bleeding complications associated with the existing anti-clotting therapies. Orally available compounds would be particularly useful for longer term therapy of patients at risk for recurrent myocardial infarction or unstable angina.

Given the role of integrins in the various disease states described above, it would be desirable to have high specificity inhibitors of particular integrins. The present invention provides such agents.

The dogma for many years was that nucleic acids had primarily an informational role. Through a method known as Systematic Evolution of Ligands by EXponential enrichment, termed the SELEX process, it has become clear that nucleic acids have three dimensional structural diversity not unlike proteins. The SELEX process is a method for the *in vitro* evolution of nucleic acid molecules with highly specific binding to target molecules and is described in U.S. Patent Application Serial No. 07/536,428, filed June 11, 1990, entitled "Systematic Evolution of Ligands by EXponential Enrichment," now abandoned, U.S. Patent No. 5,475,096, entitled "Nucleic Acid Ligands" and U.S. Patent No. 5,270,163 (see also WO 91/19813), entitled "Methods for Identifying Nucleic Acid Ligands," each of which is specifically incorporated by reference herein in its entirety. Each of these applications, collectively referred to herein as the SELEX Patent Applications, describes a fundamentally novel method for making a nucleic acid ligand to any desired target molecule. The SELEX process provides a class of products which are referred to as nucleic acid ligands or aptamers, each having a unique sequence, and which has the property of binding specifically to a desired target compound or molecule. Each SELEX-identified nucleic acid ligand is a specific ligand of a given target compound or molecule. The SELEX process is based on the unique insight that nucleic acids have sufficient capacity for forming a variety of two- and three-dimensional structures and sufficient chemical versatility available within their monomers to act as ligands (form specific binding pairs) with virtually any chemical compound, whether monomeric or

polymeric. Molecules of any size or composition can serve as targets. The SELEX method applied to the application of high affinity binding involves selection from a mixture of candidate oligonucleotides and step-wise iterations of binding, partitioning and amplification, using the same general selection scheme, to achieve virtually any desired criterion of binding affinity and selectivity. Starting from a mixture of nucleic acids, preferably comprising a segment of randomized sequence, the SELEX method includes steps of contacting the mixture with the target under conditions favorable for binding, partitioning unbound nucleic acids from those nucleic acids which have bound specifically to target molecules, dissociating the nucleic acid-target complexes, amplifying the nucleic acids dissociated from the nucleic acid-target complexes to yield a ligand-enriched mixture of nucleic acids, then reiterating the steps of binding, partitioning, dissociating and amplifying through as many cycles as desired to yield highly specific high affinity nucleic acid ligands to the target molecule.

It has been recognized by the present inventors that the SELEX method demonstrates that nucleic acids as chemical compounds can form a wide array of shapes, sizes and configurations, and are capable of a far broader repertoire of binding and other functions than those displayed by nucleic acids in biological systems.

The basic SELEX method has been modified to achieve a number of specific objectives. For example, U.S. Patent Application Serial No. 07/960,093, filed October 14, 1992, now abandoned, and U.S. Patent No. 5,707,796, both entitled "Method for Selecting Nucleic Acids on the Basis of Structure," describe the use of the SELEX process in conjunction with gel electrophoresis to select nucleic acid molecules with specific structural characteristics, such as bent DNA. U.S. Patent Application Serial No. 08/123,935, filed September 17, 1993, entitled "Photoselection of Nucleic Acid Ligands,", now abandoned, U.S. Patent No. 5,763,177, entitled "Systematic Evolution of Ligands by Exponential Enrichment: Photoselection of Nucleic Acid Ligands and Solution SELEX" and U.S. Patent Application Serial No. 09/093,293, filed June 8, 1998, entitled "Systematic Evolution of Ligands by Exponential Enrichment: Photoselection of Nucleic Acid Ligands and Solution SELEX," describe a SELEX based method for selecting nucleic acid ligands containing photoreactive groups capable of binding and/or photocrosslinking to and/or photoinactivating a target molecule. U.S. Patent No.

5,580,737, entitled "High-Affinity Nucleic Acid Ligands That Discriminate Between Theophylline and Caffeine," describes a method for identifying highly specific nucleic acid ligands able to discriminate between closely related molecules, which can be non-peptidic, termed Counter-SELEX. U.S. Patent No. 5,567,588, entitled "Systematic Evolution of Ligands by EXponential Enrichment: Solution SELEX," describes a SELEX-based method which achieves highly efficient partitioning between oligonucleotides having high and low affinity for a target molecule.

The SELEX method encompasses the identification of high-affinity nucleic acid ligands containing modified nucleotides conferring improved characteristics on the ligand, such as improved in vivo stability or improved delivery characteristics. Examples of such modifications include chemical substitutions at the ribose and/or phosphate and/or base positions. SELEX process-identified nucleic acid ligands containing modified nucleotides are described in U.S. Patent No. 5,660,985, entitled "High Affinity Nucleic Acid Ligands Containing Modified Nucleotides," that describes oligonucleotides containing nucleotide derivatives chemically modified at the 5- and 2'-positions of pyrimidines. U.S. Patent No. 5,580,737, supra, describes highly specific nucleic acid ligands containing one or more nucleotides modified with 2'-amino (2'-NH_2), 2'-fluoro (2'-F), and/or 2'-O-methyl (2'-OMe). U.S. Patent Application Serial No. 08/264,029, filed June 22, 1994, entitled "Novel Method of Preparation of Known and Novel 2' Modified Nucleosides by Intramolecular Nucleophilic Displacement," now abandoned, describes oligonucleotides containing various 2'-modified pyrimidines.

The SELEX method encompasses combining selected oligonucleotides with other selected oligonucleotides and non-oligonucleotide functional units as described in U.S. Patent No. 5,637,459, entitled "Systematic Evolution of Ligands by EXponential Enrichment: Chimeric SELEX," and U.S. Patent No. 5,683,867, entitled "Systematic Evolution of Ligands by EXponential Enrichment: Blended SELEX," respectively. These applications allow the combination of the broad array of shapes and other properties, and the efficient amplification and replication properties, of oligonucleotides with the desirable properties of other molecules.

The SELEX method further encompasses combining selected nucleic acid ligands with lipophilic compounds or non-immunogenic, high molecular weight compounds in a

diagnostic or therapeutic complex as described in U.S. Patent Application Serial No. 08/434,465, filed May 4, 1995, entitled "Nucleic Acid Ligand Complexes". Each of the above described patent applications which describe modifications of the basic SELEX procedure are specifically incorporated by reference herein in their entirety.

It is an object of the present invention to provide methods that can be used to identify nucleic acid ligands that bind with high specificity and affinity to particular integrins.

It is a further object of the present invention to obtain nucleic acid ligands to particular integrins that inhibit the ability of that integrin to bind its cognate ligand.

It is a further object of the present invention to obtain integrin inhibiting pharmaceutical compositions for controlling thrombosis, tumor angiogenesis, tumor cell migration, proliferative ocular diseases, rheumatoid arthritis, psoriasis, osteoporosis, and restenosis.

It is yet a further object of the invention to obtain imaging agents for the non-invasive detection of deep vein or arterial thrombi.

Summary of the Invention

Methods are provided for generating nucleic acid ligands to integrins, particularly to the β_3 integrins. The methods use the SELEX process for ligand generation. Particular embodiments describe the isolation of nucleic acid ligand inhibitors of both $\alpha_v\beta_3$ and $\alpha_{IIb}\beta_3$. The nucleic acid ligand inhibitors are derived from a library of 2'-fluoro-pyrimidine RNA sequences and were selected for high affinity binding to $\alpha_v\beta_3$. One of the modified nucleic acid ligands is shown to inhibit the binding of either vitronectin or fibrinogen to both of the purified integrins *in vitro*. This nucleic acid ligand binds to the surface of both resting and activated platelets with equivalent affinity and accumulates at the site of a preformed clot in an animal model of venous thrombosis.

The nucleic acid ligands provided by the invention are useful as therapeutic agents for a number of diseases including thrombosis and cancer. The nucleic acid ligands of the instant invention are also useful as diagnostic agents for thrombosis.

Brief Description of the Drawings

FIGURE 1 illustrates the binding of affinity-enriched RNA pools to immobilized $\alpha_v\beta_3$. 5'-biotinylated RNA pools were incubated at varying concentrations in 96-well microtiter plates coated with integrin $\alpha_v\beta_3$. Bound RNAs were detected via the biotin moiety by a chromogenic assay. Data are expressed in absorbance units at 405 nm as a function of input RNA concentration.

FIGURE 2 illustrates cross-reactivity of aptamer 17.16 (SEQ ID NO:60) to purified integrin $\alpha_{IIb}\beta_3$. 5'-biotinylated aptamer 17.16 was incubated at varying concentrations in microtiter wells coated with either integrin $\alpha_v\beta_3$ or $\alpha_{IIb}\beta_3$. Bound RNA was detected via the biotin moiety using a chromogenic assay. Data are expressed as the per cent of the maximum signal to normalize for differences in protein coating.

FIGURE 3 illustrates cross-reactivity of aptamer 17.16 (SEQ ID NO:60) to purified integrin $\alpha_v\beta_5$. 5'-biotinylated aptamer 17.16 or a control RNA of similar length and base composition were incubated at varying concentrations in microtiter wells coated with either $\alpha_v\beta_3$ or $\alpha_v\beta_5$. Bound RNAs were detected via the biotin moiety by a chromogenic assay. Data are expressed in absorbance units at 405 nm as a function of input RNA concentration.

FIGURES 4A-C illustrate β3 aptamer inhibition of integrin ligand binding. Biotinylated fibrinogen or vitronectin were incubated in microtiter wells coated with either integrin $\alpha_v\beta_3$ or $\alpha_{IIb}\beta_3$ in the presence or absence of varying concentrations of ligand binding competitors. Competitors included aptamer 17.16 (SEQ ID NO:60), a control RNA of similar length and base composition, a cyclic RGD peptide (cRGD, see Materials and Methods), an $\alpha_v\beta_3$-specific monoclonal antibody (LM609), or unmodified fibrinogen or vitronectin. Bound ligands were detected via biotin using a chromogenic assay. Data are expressed in absorbance units at 405 nm as a function of input competitor concentration. FIGURE 4A shows competition of vitronectin binding to immobilized $\alpha_v\beta_3$; FIGURE 4B shows competition of fibrinogen binding to immobilized $\alpha_v\beta_3$; and FIGURE 4C shows

competition of fibrinogen binding to immobilized $\alpha_{IIb}\beta_3$. An estimate of the maximum absorbance value was determined for each ligand/integrin pair in the absence of competitor. The baseline absorbance value was determined by adding 5 mM EDTA to the incubation buffer. The maximum and minimum values so determined were FIGURE 4A, 0.914/0.113; FIGURE 4B, 1.042/0.122; FIGURE 4C, 0.889/0.128.

FIGURE 5 illustrates binding of aptamer 17.16 (SEQ ID NO:60) to activated or resting human platelets. 5'-fluorescein-conjugated aptamer 17.16 or a control RNA of similar length and base composition were incubated at various concentrations with resting or thrombin-activated human platelets (10^6/mL). Incubations were at room temperature in buffered saline containing divalent cations, 0.1% BSA and 0.01% sodium azide. Mean fluorescence intensity of the sample was determined by flow cytometry both before and after the addition of EDTA to 5 mM final concentration. The difference in fluorescence intensity between the two samples (the EDTA-sensitive signal) is shown as a function of the concentration of aptamer or control RNA.

FIGURE 6 illustrates biodistribution of [^{99m}Tc]-aptamer 17.16 (SEQ ID NO:60) or control RNA in a rabbit venous clot model. A clot derived from human platelet-rich plasma was generated *in situ* by temporary isolation of the jugular vein of an anesthetized rabbit. After restoration of circulation over the clot, [^{99m}Tc]-labeled aptamer or control RNA were injected into the bloodstream of the rabbit via the ipsilateral ear vein. After one hour, the animal was sacrificed and tissues were weighed and counted in a gamma counter. Accumulation of radioactivity in various tissues is reported as the percentage of the injected dose per gram wet weight of tissue.

Detailed Description of the Preferred Embodiments

The central method utilized herein for identifying nucleic acid ligands to Integrins is called the SELEX process, an acronym for Systematic Evolution of Ligands by Exponential enrichment and involves (a) contacting the candidate mixture of nucleic acids with integrins, or expressed domains or peptides corresponding to integrins, (b) partitioning between members of said candidate mixture on the basis of affinity to

integrins, and c) amplifying the selected molecules to yield a mixture of nucleic acids enriched for nucleic acid sequences with a relatively higher affinity for binding to integrins.

Definitions

Various terms are used herein to refer to aspects of the present invention. To aid in the clarification of the description of the components of this invention, the following definitions are provided:

As used herein, "nucleic acid ligand" is a non-naturally occurring nucleic acid having a desirable action on a target. Nucleic acid ligands are often referred to as "aptamers". The term aptamer is used interchangeably with nucleic acid ligand throughout this application. A desirable action includes, but is not limited to, binding of the target, catalytically changing the target, reacting with the target in a way which modifies/alters the target or the functional activity of the target, covalently attaching to the target as in a suicide inhibitor, facilitating the reaction between the target and another molecule. In the preferred embodiment, the action is specific binding affinity for a target molecule, such target molecule being a three dimensional chemical structure other than a polynucleotide that binds to the nucleic acid ligand through a mechanism which predominantly depends on Watson/Crick base pairing or triple helix binding, wherein the nucleic acid ligand is not a nucleic acid having the known physiological function of being bound by the target molecule. In the present invention, the target is an integrin, or portions thereof. Nucleic acid ligands include nucleic acids that are identified from a candidate mixture of nucleic acids, said nucleic acid ligand being a ligand of a given target, by the method comprising: a) contacting the candidate mixture with the target, wherein nucleic acids having an increased affinity to the target relative to the candidate mixture may be partitioned from the remainder of the candidate mixture; b) partitioning the increased affinity nucleic acids from the remainder of the candidate mixture; and c) amplifying the increased affinity nucleic acids to yield a ligand-enriched mixture of nucleic acids.

As used herein, "candidate mixture" is a mixture of nucleic acids of differing sequence from which to select a desired ligand. The source of a candidate mixture can be

from naturally-occurring nucleic acids or fragments thereof, chemically synthesized nucleic acids, enzymatically synthesized nucleic acids or nucleic acids made by a combination of the foregoing techniques. In a preferred embodiment, each nucleic acid has fixed sequences surrounding a randomized region to facilitate the amplification process.

As used herein, "nucleic acid" means either DNA, RNA, single-stranded or double-stranded, and any chemical modifications thereof. Modifications include, but are not limited to, those which provide other chemical groups that incorporate additional charge, polarizability, hydrogen bonding, electrostatic interaction, and fluxionality to the nucleic acid ligand bases or to the nucleic acid ligand as a whole. Such modifications include, but are not limited to, 2'-position sugar modifications, 5-position pyrimidine modifications, 8-position purine modifications, modifications at exocyclic amines, substitution of 4-thiouridine, substitution of 5-bromo or 5-iodo-uracil; backbone modifications, methylations, unusual base-pairing combinations such as the isobases isocytidine and isoguanidine and the like. Modifications can also include 3' and 5' modifications such as capping.

"SELEX" methodology involves the combination of selection of nucleic acid ligands which interact with a target in a desirable manner, for example binding to a protein, with amplification of those selected nucleic acids. Optional iterative cycling of the selection/amplification steps allows selection of one or a small number of nucleic acids which interact most strongly with the target from a pool which contains a very large number of nucleic acids. Cycling of the selection/amplification procedure is continued until a selected goal is achieved. In the present invention, the SELEX methodology is employed to obtain nucleic acid ligands to integrins.

The SELEX methodology is described in the SELEX Patent Applications.

"SELEX target" or "target" means any compound or molecule of interest for which a ligand is desired. A target can be a protein, peptide, carbohydrate, polysaccharide, glycoprotein, hormone, receptor, antigen, antibody, virus, substrate, metabolite, transition state analog, cofactor, inhibitor, drug, dye, nutrient, growth factor, etc. without limitation. In this application, the SELEX targets are integrins.

As used herein, "solid support" is defined as any surface to which molecules may be attached through either covalent or non-covalent bonds. This includes, but is not limited to, membranes, microtiter plates, magnetic beads, charged paper, nylon, Langmuir-Bodgett films, functionalized glass, germanium, silicon, PTFE, polystyrene, gallium arsenide, gold, and silver. Any other material known in the art that is capable of having functional groups such as amino, carboxyl, thiol or hydroxyl incorporated on its surface, is also contemplated. This includes surfaces with any topology, including, but not limited to, spherical surfaces and grooved surfaces.

Note that throughout this application, various references are cited. Every reference cited herein is specifically incorporated in its entirety.

A. Preparing nucleic acid ligands to integrins.

In the preferred embodiment, the nucleic acid ligands of the present invention are derived from the SELEX methodology. The SELEX process is described in U.S. Patent Application Serial No. 07/536,428, entitled "Systematic Evolution of Ligands by Exponential Enrichment," now abandoned, U.S. Patent No. 5,475,096, entitled "Nucleic Acid Ligands," and U.S. Patent No. 5,270,163 (see also WO 91/19813) entitled "Methods for Identifying Nucleic Acid Ligands." These applications, each specifically incorporated herein by reference, are collectively called the SELEX Patent Applications.

The SELEX process provides a class of products which are nucleic acid molecules, each having a unique sequence, and each of which has the property of binding specifically to a desired target compound or molecule. Target molecules are preferably proteins, but can also include among others carbohydrates, peptidoglycans and a variety of small molecules. SELEX methodology can also be used to target biological structures, such as cell surfaces or viruses, through specific interaction with a molecule that is an integral part of that biological structure.

In its most basic form, the SELEX process may be defined by the following series of steps:

1) A candidate mixture of nucleic acids of differing sequence is prepared. The candidate mixture generally includes regions of fixed sequences (i.e., each of the members of the candidate mixture contains the same sequences in the same location) and

regions of randomized sequences. The fixed sequence regions are selected either: (a) to assist in the amplification steps described below, (b) to mimic a sequence known to bind to the target, or (c) to enhance the concentration of a given structural arrangement of the nucleic acids in the candidate mixture. The randomized sequences can be totally randomized (i.e., the probability of finding a base at any position being one in four) or only partially randomized (e.g., the probability of finding a base at any location can be selected at any level between 0 and 100 percent).

2) The candidate mixture is contacted with the selected target under conditions favorable for binding between the target and members of the candidate mixture. Under these circumstances, the interaction between the target and the nucleic acids of the candidate mixture can be considered as forming nucleic acid-target pairs between the target and those nucleic acids having the strongest affinity for the target.

3) The nucleic acids with the highest affinity for the target are partitioned from those nucleic acids with lesser affinity to the target. Because only an extremely small number of sequences (and possibly only one molecule of nucleic acid) corresponding to the highest affinity nucleic acids exist in the candidate mixture, it is generally desirable to set the partitioning criteria so that a significant amount of the nucleic acids in the candidate mixture (approximately 5-50%) are retained during partitioning.

4) Those nucleic acids selected during partitioning as having the relatively higher affinity for the target are then amplified to create a new candidate mixture that is enriched in nucleic acids having a relatively higher affinity for the target.

5) By repeating the partitioning and amplifying steps above, the newly formed candidate mixture contains fewer and fewer unique sequences, and the average degree of affinity of the nucleic acids to the target will generally increase. Taken to its extreme, the SELEX process will yield a candidate mixture containing one or a small number of unique nucleic acids representing those nucleic acids from the original candidate mixture having the highest affinity to the target molecule.

The basic SELEX method has been modified to achieve a number of specific objectives. For example, U.S. Patent Application Serial No. 07/960,093, filed October 14, 1992, now abandoned, and U.S. Patent No. 5,707,796 both entitled "Method for Selecting Nucleic Acids on the Basis of Structure," describe the use of the SELEX

process in conjunction with gel electrophoresis to select nucleic acid molecules with specific structural characteristics, such as bent DNA. U.S. Patent Application Serial No. 08/123,935, filed September 17, 1993, entitled "Photoselection of Nucleic Acid Ligands," now abandoned, U.S. Patent No. 5,763,177, entitled "Systematic Evolution of Ligands by Exponential Enrichment: Photoselection of Nucleic Acid Ligands and Solution SELEX" and U.S. Patent Application Serial No. 09/093,293, filed June 8, 1998, entitled "Systematic Evolution of Ligands by Exponential Enrichment: Photoselection of Nucleic Acid Ligands and Solution SELEX," all describe a SELEX based method for selecting nucleic acid ligands containing photoreactive groups capable of binding and/or photocrosslinking to and/or photoinactivating a target molecule. U.S. Patent No. 5,580,737, entitled "High-Affinity Nucleic Acid Ligands That Discriminate Between Theophylline and Caffeine," describes a method for identifying highly specific nucleic acid ligands able to discriminate between closely related molecules, termed Counter-SELEX. U.S. Patent No. 5,567,588, entitled "Systematic Evolution of Ligands by Exponential Enrichment: Solution SELEX," describes a SELEX-based method which achieves highly efficient partitioning between oligonucleotides having high and low affinity for a target molecule. U.S. Patent No. 5,496,938, entitled "Nucleic Acid Ligands to HIV-RT and HIV-1 Rev," describes methods for obtaining improved nucleic acid ligands after SELEX has been performed. U.S. Patent No. 5,705,337, entitled "Systematic Evolution of Ligands by Exponential Enrichment: Chemi-SELEX," describes methods for covalently linking a ligand to its target.

The SELEX method encompasses the identification of high-affinity nucleic acid ligands containing modified nucleotides conferring improved characteristics on the ligand, such as improved in vivo stability or improved delivery characteristics. Examples of such modifications include chemical substitutions at the ribose and/or phosphate and/or base positions. SELEX-identified nucleic acid ligands containing modified nucleotides are described in U.S. Patent No. 5,660,985, entitled "High Affinity Nucleic Acid Ligands Containing Modified Nucleotides," that describes oligonucleotides containing nucleotide derivatives chemically modified at the 5- and 2'-positions of pyrimidines. U.S. Patent No. 5,637,459, supra, describes highly specific nucleic acid ligands containing one or more nucleotides modified with 2'-amino (2'-NH_2), 2'-fluoro

(2'-F), and/or 2'-O-methyl (2'-OMe). U.S. Patent Application Serial No. 08/264,029, filed June 22, 1994, entitled "Novel Method of Preparation of Known and Novel 2' Modified Nucleosides by Intramolecular Nucleophilic Displacement," now abandoned, describes oligonucleotides containing various 2'-modified pyrimidines.

The SELEX method encompasses combining selected oligonucleotides with other selected oligonucleotides and non-oligonucleotide functional units as described in U.S. Patent No. 5,637,459, entitled "Systematic Evolution of Ligands by Exponential Enrichment: Chimeric SELEX," and U.S. Patent No. 5,683,867, entitled "Systematic Evolution of Ligands by Exponential Enrichment: Blended SELEX," respectively. These applications allow the combination of the broad array of shapes and other properties, and the efficient amplification and replication properties, of oligonucleotides with the desirable properties of other molecules.

In U.S. Patent No. 5,496,938 methods are described for obtaining improved nucleic acid ligands after the SELEX process has been performed. This patent, entitled Nucleic Acid Ligands to HIV-RT and HIV-1 Rev, is specifically incorporated herein by reference.

One potential problem encountered in the diagnostic use of nucleic acids is that oligonucleotides in their phosphodiester form may be quickly degraded in body fluids by intracellular and extracellular enzymes such as endonucleases and exonucleases before the desired effect is manifest. Certain chemical modifications of the nucleic acid ligand can be made to increase the in vivo stability of the nucleic acid ligand or to enhance or to mediate the delivery of the nucleic acid ligand. See, e.g., U.S. Patent Application Serial No. 08/117,991, filed September 8, 1993, now abandoned, and U.S. Patent No. 5,660,985, both entitled "High Affinity Nucleic Acid Ligands Containing Modified Nucleotides", and the U.S. Patent Application entitled "Transcription-Free SELEX", U.S. Patent Application Serial No. 09/356,578, filed July 28, 1999, each of which is specifically incorporated herein by reference. Modifications of the nucleic acid ligands contemplated in this invention include, but are not limited to, those which provide other chemical groups that incorporate additional charge, polarizability, hydrophobicity, hydrogen bonding, electrostatic interaction, and fluxionality to the nucleic acid ligand bases or to the nucleic acid ligand as a whole. Such modifications include, but are not

limited to, 2'-position sugar modifications, 5-position pyrimidine modifications, 8-position purine modifications, modifications at exocyclic amines, substitution of 4-thiouridine, substitution of 5-bromo or 5-iodo-uracil; backbone modifications, phosphorothioate or alkyl phosphate modifications, methylations, unusual base-pairing combinations such as the isobases isocytidine and isoguanidine and the like. Modifications can also include 3' and 5' modifications such as capping. In preferred embodiments of the instant invention, the nucleic acid ligands are RNA molecules that are 2'-fluoro (2'-F) modified on the sugar moiety of pyrimidine residues.

The modifications can be pre- or post-SELEX process modifications. Pre-SELEX process modifications yield nucleic acid ligands with both specificity for their SELEX target and improved in vivo stability. Post-SELEX process modifications made to 2'-OH nucleic acid ligands can result in improved in vivo stability without adversely affecting the binding capacity of the nucleic acid ligand.

Other modifications are known to one of ordinary skill in the art. Such modifications may be made post-SELEX process (modification of previously identified unmodified ligands) or by incorporation into the SELEX process.

The nucleic acid ligands of the invention are prepared through the SELEX methodology that is outlined above and thoroughly enabled in the SELEX applications incorporated herein by reference in their entirety. The SELEX process can be performed using purified integrins, or fragments thereof as a target. Alternatively, full-length integrins, or discrete domains of integrins, can be produced in a suitable expression system. Alternatively, the SELEX process can be performed using as a target a synthetic peptide that includes sequences found in an integrin. Determination of the precise number of amino acids needed for the optimal nucleic acid ligand is routine experimentation for skilled artisans.

In some embodiments, the nucleic acid ligands become covalently attached to their targets upon irradiation of the nucleic acid ligand with light having a selected wavelength. Methods for obtaining such nucleic acid ligands are detailed in U.S. Patent Application Serial No. 08/123,935, filed September 17, 1993, entitled "Photoselection of Nucleic Acid Ligands," now abandoned, U.S. Patent No. 5,763,177, entitled "Systematic Evolution of Ligands by Exponential Enrichment: Photoselection of Nucleic Acid

Ligands and Solution SELEX" and U.S. Patent Application Serial No. 09/093,293, filed June 8 1998, entitled "Systematic Evolution of Ligands by Exponential Enrichment: Photoselection of Nucleic Acid Ligands and Solution SELEX," each of which is specifically incorporated herein by reference in its entirety.

In preferred embodiments, the SELEX process is carried out using integrins attached to polystyrene beads. A candidate mixture of single stranded RNA molecules is then contacted with the beads. In especially preferred embodiments, the single stranded RNA molecules have a 2'-fluoro modification on C and U residues, rather than a 2'-OH group. After incubation for a predetermined time at a selected temperature, the beads are washed to remove unbound candidate nucleic acid ligand. The nucleic acid ligand that binds to the integrin is then released into solution, then reverse transcribed by reverse transcriptase and amplified using the Polymerase Chain Reaction. The amplified candidate mixture is then used to begin the next round of the SELEX process. Example 2 illustrates one possible way of performing the SELEX process using integrins as targets.

In preferred embodiments, the nucleic acid ligands thus obtained are assayed for their ability to inhibit the interaction of the integrin with its cognate ligand. In one embodiment, this is performed by first coating microtiter plates with the appropriate integrin(s). A ligand for the integrin, such as vitronectin or fibrinogen, is then biotinylated and contacted with the coated integrin in the presence of the nucleic acid ligand to be assayed. After incubation for a suitable period of time, the microtiter plate is washed, and the amount of vitronectin or fibrinogen binding to integrin is quantitated by adding a streptavidin-alkaline phosphatase conjugate, followed by a colorimetric substrate for alkaline phosphatase, such as p-nitrophenyl phosphate. The alkaline phosphatase signal in each well of the plate is thus inversely proportional to the effectiveness of the nucleic acid ligand as an inhibitor of the interaction between the bound integrin and its cognate ligand.

In other embodiments, the nucleic acid ligands can be analyzed using binding to human platelets as an assay. This can be done, for example, by fluorescently labelling the nucleic acid ligand by any of the numerous techniques known in the art. The fluorescent nucleic acid ligand can then be contacted with platelets, and the amount of nucleic acid ligand can be quantitated using Fluorescence Activated Cell Sorting (FACS).

The distribution of the nucleic acid ligands of the instant invention can also be studied *in vivo*. In some embodiments, nucleic acid ligands are labelled with a radiolabel used in the art of radioimaging. For example, a nucleic acid ligand can be conjugated to the isotope ^{99m}Tc using one of a number of techniques known in the art. The radiolabeled nucleic acid can then be studied in an animal model of venous thrombosis. For example, a human blood clot can be generated in rabbit vein by first isolating the vein *in situ* by ligation, and then infusing the vein with human platelet-rich plasma and heparin to induce the formation of a blood clot. Blood flow through the vein is then re-established, and the radiolabeled nucleic acid ligand is introduced into the animals blood supply. The distribution of the radiolabeled nucleic acid ligand can then be studied in the rabbit's tissues to determine whether the nucleic acid ligand has accumulated in the clot, rather than in other areas.

The nucleic acid ligands provided by the instant invention have a number of potential uses as therapeutic and diagnostic agents. In some embodiments, nucleic acid ligands that inhibit the interaction between platelet-expressed integrins and their cognate ligands are administered, along with pharmaceutically accepted excipients, in order to prevent the formation of blood clots in patients susceptible to deep vein thrombosis. In other embodiments, the nucleic acid ligands are used to treat acute thrombosis formation during and following percutaneous coronary intervention. In still other embodiments, the nucleic acid ligands of the invention are used to treat patients with acute coronary syndromes such as unstable angina or myocardial infarction.

In other embodiments, radiolabeled nucleic acid ligands to platelet-expressed integrins are administered to individuals who are to undergo major surgery, or have suffered major trauma. Such nucleic acid ligands can function as imaging agents for the detection of thrombi, by showing sites in the body where large aggregations of platelets are present. If a thrombosis is detected by radioimaging at a critical site in the body, then anticoagulant and thrombolytic treatment--including treatment with the inhibitory nucleic acid ligands of the instant invention-- can be given locally. The advantage of using such a nucleic acid ligand imaging agent is that the anticoagulant and thrombolytic treatments--which can cause harm if administered prophylactically by allowing internal bleeding to continue without efficient clotting--can be given only to those individuals who definitely

have a dangerous thrombosis. Moreover, these treatments can be specifically injected at the site where the thrombosis has been detected by the nucleic acid ligand, instead of injecting higher concentrations into the bloodstream in the hope that some active agent will be carried to all potential sites of thrombosis.

Nucleic acid ligands to $\alpha_v\beta_3$ integrin can be used to inhibit tumor growth and metastasis. They can also be used to treat ocular diseases including, but not limited to, diabetic retinopathy, retinopathy of prematurity, and macular degeneration. Other diseases for which $\alpha_v\beta_3$ nucleic acid ligands are useful therapeutic agents include, but are not limited to, endometriosis, psoriasis, rheumatoid arthritis, stroke, osteoporosis, and restenosis.

Examples

The following examples are given for illustrative purposes only. They are not to be taken as limiting the scope of the invention in any way.

Example 1. Isolation of integrins and integrin ligands

$\alpha_v\beta_3$ integrin was isolated from human placenta and purified by immunoaffinity chromatography essentially as described by (Smith and Cheresh (1988) J. Biol. Chem. 263:18726-31). In brief, human placentas were diced and the tissue fragments were extracted in a buffer containing 100 mM octyl-β-D-glucopyranoside detergent (Calbiochem, San Diego, CA). The extract was cleared by centrifugation and applied to an immunoaffinity column ($\alpha_v\beta_3$-specific monoclonal antibody LM609 affixed to Affi-Gel 10, (Chemicon International, Inc., Temecula, CA)). Protein bound to the column was eluted with a low-pH buffer and fractions were immediately neutralized and analyzed for integrin content by SDS-polyacrylamide gel electrophoresis. Integrin-containing fractions were pooled and aliquots of the purified material were stored at -80°C. Purified human $\alpha_v\beta_3$ was also purchased from Chemicon International, Inc, as was human $\alpha_v\beta_5$ integrin. $\alpha_{IIb}\beta_3$ and fibrinogen were purchased from Enzyme Research Laboratories, Inc. (South Bend, IN). Vitronectin was purified from outdated human plasma according to the procedure of (Yatohgo *et al.* (1988) Cell Struct. Func. 13:281-92), using heparin affinity chromatography.

Example 2. Generating nucleic acid ligands to integrins using the SELEX method

A DNA template library of sequence:

5'-*ttatacgactcactata*gggagacaagaataaacgctcaannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnttcgacaggaggctcacaacaggc-3' (SEQ ID NO:1)

was prepared by chemical synthesis. The italicized nucleotides correspond to a T7 RNA polymerase promoter. There are 40 n residues (a,g,t, or c). A short DNA primer "3N8":

5'- gcctgttgtgagcctcctgtcgaa-3' (SEQ ID NO:2)

was annealed to the template and extended using Klenow DNA polymerase (New England Biolabs, Beverly, MA). The double-stranded DNA product served as a product for T7 RNA polymerase transcription (enzyme obtained from Enzyco, Inc., Denver, CO) to generate a library of random-sequence RNAs. 2'-fluoro-CTP and -UTP were used in place of the 2'-OH-pyrimidines.

For application of the SELEX process to $\alpha_v\beta_3$ integrin, the purified protein was diluted 1000-fold from detergent-containing storage buffer into 50 mM MES (2-[N-morpholino]ethanesulfonic acid), pH 6.1, 150 mM NaCl, 2 mM $CaCl_2$, to a final concentration of approximately 0.2 μg/mL. 3.2 μ polystyrene particles (IDEXX Laboratories, Inc., Westbrook, ME) were added to the diluted protein and the mixture was rotated overnight at 4°C. The beads were collected by centrifugation and blocked by incubation in 3% BSA in MES buffer (above) for one hour at room temperature. Blocked beads were washed several times by resuspension in binding buffer (50 mM Tris.HCl, pH 7.4 (at 37°C), 145 mM NaCl, 4 mM KCl, 1 mM $MgCl_2$, 2 mM $CaCl_2$, 0.1 mM $MnCl_2$, 0.01% BSA). For one round of selection, integrin-coated beads were mixed with RNA and rotated at 37°C for 4 hours to allow equilibration of the RNA with the immobilized protein. The beads were then collected by centrifugation and washed at least 5 times in binding buffer by rapid resuspension and pelleting, without additional incubation. RNAs that remained bound to the beads were eluted overnight at 37°C in binding buffer plus 100 μM cyclic RGD peptide ("cRGD") (GPenGRGDSPCA, Life Technologies, Gibco BRL, Gaithersburg, MD). Eluted RNAs were extracted with phenol, then chloroform:isoamyl alcohol (24:1), and ethanol precipitated. The RNA pellet was resuspended and annealed to primer 3N8 for reverse transcription using avian myeloblastosis virus reverse transcriptase (Life Sciences, Inc., St. Petersburg, FL). The

cDNA pool was amplified by the polymerase chain reaction using the 3N8 primer and primer "5N8": 5'-taatacgactcactatagggagacaagaataaacgctcaa-3' (SEQ ID NO:3) and T. aquaticus DNA polymerase (Perkin Elmer-Cetus, Foster City, CA). Transcription of the PCR product generated an RNA pool to initiate a new round of selection. For the first round of selection 1 nmol of RNA (approximately 6 x 10^{14} sequences) was incubated at 2 μM concentration with a volume of bead suspension equivalent to 50 pmol of protein (assuming all the integrin had adsorbed to the beads). In subsequent rounds, the concentration of RNA and protein-coated beads were both reduced to demand higher affinity binding interactions.

The affinity of individual RNAs and RNA pools for $\alpha_v\beta_3$ was determined by titration of biotinylated RNA with a small quantity of immobilized integrin. Bound RNA was detected through the biotin moiety. Biotinylated RNA was prepared according to standard transcription protocols, but including a 5-fold molar excess of a 5'-biotin-modified GMP over GTP in the reaction mixture. Methods for synthesizing 5'-biotin-modified guanosine nucleotides are described in WO 98/30720 entitled "Bioconjugation of Oligonucleotides," specifically incorporated herein by reference in its entirety. The modified nucleotide is incorporated at the 5' end of the transcript in proportion to its representation in the guanosine pool. 96-well microtiter plates (Immulon 2, Dynatech Laboratories, Inc., Chantilly, VA) were coated overnight at 4°C with 100 μL purified $\alpha_v\beta_3$ at a concentration of 0.25 μg/mL in 20 mM TrisHCl, pH 7.5, 150 mM NaCl, 1 mM $MgCl_2$, 2 mM $CaCl_2$, 0.1 mM $MnCl_2$. Coating concentrations were 0.8 μg/mL for $\alpha_{IIb}\beta_3$ and 0.3 μg/mL for $\alpha_v\beta_5$. Wells were blocked with 200 μL of a solution of 3% BSA in the same buffer (1 hour at room temperature) then rinsed 3 times with 200 μL binding buffer (50 mM TrisHCl, pH 7.5, 137 mM NaCl, 2.7 mM KCl, 1 mM $MgCl_2$, 2 mM $CaCl_2$, 0.1 mM $MnCl_2$, 0.1% BSA). Individual RNAs or RNA pools were denatured briefly at 93°C in binding buffer without divalent cations or BSA, then serially diluted in the same buffer. 50 μL binding buffer containing 2X-concentrations of divalent cations and BSA were added to each well, followed by 50 μL RNA dilution. RNAs were allowed to incubate in the integrin-coated wells at 37°C for 30-60 minutes. Unbound RNAs were removed by 3 rapid washes in binding buffer. To detect bound RNA, 100 μL of a 1:2500

dilution in binding buffer of streptavidin-alkaline phosphatase conjugate (Calbiochem) were incubated in each well for 30 minutes at room temperature, followed by three rapid washes, as above. 100 μL/well p-nitrophenyl phosphate (Sigma Chemical Co., St. Louis, MO) was added and incubated at room temperature for 30 minutes. Color development was monitored by absorbance at 405 nm. Binding data were fit to an equation that describes the fraction of RNA or protein bound as a function of K_D, and the total concentrations of RNA and protein in the binding reaction for both monophasic and biphasic binding behavior (Green *et al.* (1996) Biochem. 35:14413-24). A control RNA corresponding to a sequence-scrambled version of aptamer 7.24:

5'-gggagacaagaauaaucgcucaacguugaaugcugcauuauggaguauugaccgcuacaucccuucgaca ggaggcucacaacaggc-3' (SEQ ID NO:4)

was used to monitor non-specific binding of RNA under the conditions of the assay.

After seven rounds of the SELEX process, the amount of RNA specifically bound to the integrin-coated beads had increased substantially (data not shown). Although immobilized $\alpha_v\beta_3$ showed no detectable affinity for random sequence RNA, the Round 7 RNA pool bound with an equilibrium dissociation constant (K_D) of approximately 4×10^{-7} M (FIGURE 1). The Round 7 affinity-enriched pool was cloned and sequences were determined for individual molecules in the mixture. Of 92 sequences obtained, 35 (38%) were very highly related to one another, in many cases differing at no more than a single base position. These sequences are collectively referred to as "Family 1." It is likely that many if not most of these RNAs derived from a single precursor as a result of errors in replication during the RT and PCR steps. Another 25 sequences (27%) shared a short motif (CCUGCC) that defined a second sequence family ("Family 2"). The remaining 32 sequences (35%) were not obviously related to sequences in Families 1 or 2 and were thus termed "orphan" sequences. The large percentage of orphan sequences in the round 7 pool suggested that a great deal of sequence complexity remained in the population. Therefore, the SELEX process was continued in the hope of further enriching for high affinity sequences whose representation in the round 7 pool may have been low. Indeed, a substantial improvement in the affinity of the RNA pool was observed after 8 additional rounds of affinity selection (Round 15, FIGURE 1). No further improvement was seen after two more rounds of selection (Round 17, FIGURE

1), so clones were isolated from the Round 15 and Round 17 RNA pools and the sequences of individual isolates were compared to those obtained at Round 7. Twenty-seven of 39 sequences derived from the Round 15 pool (69%) were members of the highly conserved sequence family, Family 1. Three sequences (8%) could be grouped with Family 2 and 9 sequences (23%) were orphans. All of the 18 sequences isolated from the Round 17 pool were members of sequence Family 1. Thus, in this case, additional rounds of the SELEX process served to focus the RNA population on a single high-affinity sequence family that was already predominate at Round 7.

Table 1 shows the sequences of the major family of 2'-F-pyrimidine RNAs with high affinity for $\alpha_v\beta_3$ (Family 1). Clone names indicate the selected RNA pool from which each sequence was derived (round 7, round 15 or round 17) followed by a unique clone number. Note that in several cases identical sequences were isolated from different RNA pools; in these cases, both clone names are given. (Clones 17.12A and B were isolated as end-to-end inserts in a single plasmid.) Numbers in parentheses indicate the frequency with which a particular sequence was isolated; if no number is given the clone was obtained only once from the selected RNA pool. Sequences of the 5' and 3' fixed sequence regions common to all of the clones are shown at the top in lower case letters. Gaps have been inserted into many of the sequences to highlight the strong sequence conservation among most of the clones. The length of the random sequence region is shown for each RNA, as well as an estimate of the K_D for binding to immobilized $\alpha_v\beta_3$, where it was determined (ND = not determined). The K_D value provided is generally based on one or the average of two determinations. Family 2 sequences isolated from the αvβ3 SELEX are shown in Table 2. The short motif (CCUGCC) held in common among all the sequences is indicated in boldface letters. In Table 3, sequences with no obvious relationship to Families 1 or 2 are shown. Groups of similar sequences with only two (7.41 and 7.93) or three (7.11, 7.82 and 7.101) members are also included in Table 3.

The substantial affinity improvement between rounds 7 and 15 must be due in part to the loss of lower affinity species from the population; however, the introduction of and selection for higher affinity sequence variants of Family 1 may also have contributed to the overall affinity enrichment of the pool. While the affinity of relatively few

sequences from the Round 7 pool were measured, their affinities for immobilized $\alpha_v\beta_3$ were generally less than that of RNAs derived from Rounds 15 and 17 (Tables 1-3).

Example 3. Specificity of the nucleic acid ligands to integrins

In general, aptamers selected for high-affinity binding to a particular target protein show relatively weak binding to other related proteins, except in cases where the degree of homology is very high (for example, see (Green *et al.* (1996) Biochem. 35:14413-24; Ruckman *et al.* (1998) J. Biol. Chem. 273:20556-67)). Significant homology exists within the families of integrin alpha and beta sub-units, and both alpha and beta sub-units are shared among members of the integrin superfamily. Thus, it was of interest to assess the relative affinity of the $\alpha_v\beta_3$ aptamers for closely related integrins. The affinities were determined using the methods described above. The Family 1 aptamer 17.16 (SEQ ID NO:60) was chosen as a representative of the major sequence family. FIGURE 2 shows that aptamer 17.16 bound with identical affinity to purified, immobilized $\alpha_v\beta_3$ and to the platelet integrin, $\alpha_{IIb}\beta_3$ in a 96-well plate binding assay. Although these two proteins share the β_3 sub-unit in common, an alignment of the α_v and α_{IIB} amino acid sequences shows only 36% overall sequence identity (Fitzgerald *et al.* (1987) Biochem. 26:8158-65). Short stretches of exact sequence identity, 5 to 9 amino acids in length, do occur, primarily within four putative calcium-binding domains of each α sub-unit. Binding of aptamer 17.16 to integrin $\alpha_v\beta_5$ was also tested. The β_5 sub-unit shares 56% sequence identity with β_3 and is more closely related to β_3 than other members of the beta sub-unit family (McLean *et al.* (1990) J. Biol. Chem. 265:17126-31; Suzuki *et al.* (1990) Proc. Nat. Acad. Sci. 87:5354-8). No aptamer binding to immobilized integrin $\alpha_v\beta_5$ was observed (FIGURE 3), although an α_v-specific antibody detected the presence of $\alpha_v\beta_5$ protein adsorbed to the surface of the well (data not shown). Together, these data strongly suggest that aptamer 17.16, and by extension the other members of sequence Family 1, bind primarily to the β_3 sub-unit of $\alpha_v\beta_3$. Furthermore, the high-affinity binding of the aptamer to the platelet integrin, $\alpha_{IIb}\beta_3$ extends its range of potential application to indications involving detection of platelets or inhibition of their function.

Example 4. Aptamer inhibition of ligand binding to purified integrins

While the SELEX process identifies RNA sequences with high affinity for a particular target, the procedure used in this example was designed to bias for the recovery of ligand binding site inhibitors by the inclusion of a cRGD peptide competitor in the elution buffer. To test whether aptamer 17.16 could block the ligand binding site of $\alpha_v\beta_3$ or $\alpha_{IIb}\beta_3$, purified vitronectin and fibrinogen were biotinylated and incubated with one or both of the immobilized integrins in the presence or absence of varying concentrations of the aptamer or a non-binding control RNA. This was done as follows: purified integrin ligands, vitronectin and fibrinogen, were biotinylated according to (Smith *et al.* (1990) J. Biol. Chem. 265:12267-71). Briefly, proteins were dialyzed into 0.1 M $NaHCO_3$, 0.1 M NaCl. N-hydroxysuccinimido-LC-biotin (Pierce) was dissolved at 1 mg/mL in DMSO and added to the protein at a ratio of 0.1 mg biotin per 1 mg protein. The reaction was allowed to rotate at room temperature for 2 hours. Biotinylated proteins were dialyzed into phosphate-buffered saline and their concentrations determined by absorbance at 280 nm. 96-well microtiter plates were coated as described above with either $\alpha_v\beta_3$ or $\alpha_{IIb}\beta_3$ and blocked with BSA. A fixed concentration of biotinylated ligand (fibrinogen: 6 nM final; vitronectin: 10 nM final) was pre-mixed in binding buffer (see "Measurement of Aptamer Binding Affinities," above) with varying concentrations of aptamer, control RNA, cyclic RGD peptide, antibody, or unmodified ligand. The mixtures were incubated in the integrin-coated wells for 60 minutes at room temperature. After washing, bound biotinylated ligand was detected by addition of 100 µL/well 1:500 dilution streptavidin-alkaline phosphatase conjugate (Calbiochem) (30 minutes at room temperature) followed by 100 µL/well p-nitrophenyl phosphate, as described above. Absorbance was read at 405 nm. The data were fit to an equation that describes mutually exclusive binding of two ligands to a single target species (Gill *et al.* (1991) J. Mol. Biol. 220:307-24). The concentration of competitor that inhibited 50% of the maximum signal above background (IC_{50}) was determined from the fitted curve.

Known ligand binding inhibitors, including an RGD peptide and the $\alpha_v\beta_3$-specific antibody LM609, were included as positive controls for the assay. FIGURE 4A shows inhibition of biotinylated vitronectin binding to immobilized $\alpha_v\beta_3$. Aptamer 17.16

inhibited the binding interaction with an IC_{50} of 4.7 nM while the control RNA showed no inhibition. By comparison, the IC_{50} of RGD peptide inhibition was 1.4 nM and that of LM609 was 2.7 nM. Unmodified vitronectin inhibited the binding of the biotinylated material with an IC_{50} of 59 nM. Similar data were obtained for aptamer inhibition of fibrinogen binding to $\alpha_v\beta_3$ (FIGURE 4B) and for fibrinogen binding to $\alpha_{IIb}\beta_3$ (FIGURE 4C). IC_{50} values for the data in FIGURE 4B were: 17.16, 9.5 nM; control RNA, not measurable; RGD peptide, 1.0 nM; LM609, 6.3 nM; unmodified fibrinogen, 43 nM. IC_{50} values for FIGURE 4C were: 17.16, 6.5 nM; control RNA, not measurable; RGD peptide, 21 nM; unmodified fibrinogen, 15 nM. Thus, aptamer 17.16 is an effective competitor of β_3 integrin ligand binding and, on a molar basis, has an inhibitory potency nearly equivalent to that of a bivalent antibody.

Example 5. Nucleic acid ligand binding to human platelets

Aptamer 17.16 (SEQ ID NO:60) was selected for binding to purified human $\alpha_v\beta_3$ adsorbed to the surface of a polystyrene bead. *In vitro* assays to measure the affinity of the aptamer for purified β_3 integrins were also done in the context of hydrophobically-adsorbed protein. Thus, an important test of aptamer function was to determine its capacity to bind to native protein on the surface of cells. Human platelets were chosen for this purpose because of their ease of isolation and their high level of expression of integrin $\alpha_{IIb}\beta_3$. Because $\alpha_{IIb}\beta_3$ undergoes a conformational change upon platelet activation, binding of the aptamer to both resting and thrombin-activated platelets was tested. This was done as follow: fluorescein-conjugated RNA was prepared according to (Davis *et al.* (1998) Nuc. Acids Res. 26:3915-24). Briefly, RNA was transcribed in the presence of a 5-fold molar excess of the initiator nucleotide guanosine-5'-O-(2-thiodiphosphate) (Calciochem), followed by conjugation of the gel-purified RNA to 5-iodoacetamidofluorescein (Pierce, Rockford, IL). Platelet-rich plasma was prepared from freshly-drawn citrated human blood by centrifugation at 1000 rpm for 15 minutes in a table top centrifuge. For activated platelets, cells were incubated for 15 minutes at room temperature at 2 x 10^7/mL in calcium- and magnesium-free Dulbecco's PBS with 2.5 U/mL thrombin and 5 mM Gly-Pro-Arg-Pro (GPRP) to inhibit platelet aggregation. Cells were diluted 1:10 into binding buffer (20 mM HEPES, pH 7.5, 111 mM NaCl, 5

mM KCl, 1 mM $MgCl_2$, 1 mM $CaCl_2$, 0.1% BSA, 0.01% sodium azide). Resting cells were diluted similarly, without exposure to thrombin or GPRP. The activation state of resting and thrombin-treated cells was monitored by staining with fluorophore-conjugated antibodies to CD61 (β_3 integrin subunit), which binds to all platelets, and to CD62 (P-selectin), a marker of platelet activation. Antibodies were obtained from Becton-Dickinson Immunocytometry Systems, San Jose, CA. Fluorescein-conjugated RNAs were diluted in water to 4 μM and denatured briefly at 93°C, then diluted to 2 μM with 2X-concentrated binding buffer. RNAs were then serially diluted in binding buffer. Each dilution was mixed 1:1 with resting or activated platelets and allowed to incubate in the dark at room temperature for 30 minutes. The incubation mixtures were applied directly to a Becton Dickinson FACSCalibur flow cytometer to determine the mean fluorescence intensity of the sample. Under such equilibrium binding conditions, an estimate of the K_D for aptamer binding to the cell surface integrin could be obtained.

Non-specific RNA binding to platelets was measured using a control RNA of similar length and base composition to aptamer 17.16. Non-specific binding became significant at concentrations above approximately 100 nM. Specific binding of the aptamer was distinguished from non-specific binding by the addition of 5 mM EDTA to the sample: EDTA had no effect on the binding of the control RNA but reduced aptamer binding to the level of the control. Specific binding of the aptamer was thus defined as the difference between the fluorescence intensity of the sample before the addition of EDTA (specific + non-specific) and the fluorescence intensity after the addition of EDTA (non-specific only).

FIGURE 5 shows representative data for the EDTA-sensitive component of aptamer binding to both resting and thrombin-activated human platelets. The maximum binding signal is approximately 2-fold higher to activated platelets, consistent with the slightly higher level of $\alpha_{IIb}\beta_3$ on such cells (Wagner *et al.* (1996) Blood 88:907-14). However, the estimated K_D for aptamer binding to platelets was approximately 10 nM for both cell populations, equivalent to the value determined for binding *in vitro* to purified $\alpha_{IIb}\beta_3$. Furthermore, aptamer 17.16 binds to both resting and activated platelets with an affinity equivalent to that reported for Reopro (abciximab, chimeric 7E3 Fab), an approved $\alpha_{IIb}\beta_3$ antagonist (Mousa *et al.* (1998) J. Pharm. Exp. Ther. 286:1277-84).

Example 6. Nucleic acid ligand biodistribution in rabbit venous clot model

To explore the application of a β_3-specific aptamer in clot imaging, aptamer 17.16 was labeled at the 5' end with technitium-99m (^{99m}Tc) and its biodistribution was monitored in a rabbit model of venous thrombosis. In this model, a clot is generated *in situ* in the isolated jugular vein of a rabbit from human platelet-rich plasma. Blood flow across the clot is re-established and the radiolabeled aptamer (or a non-binding control RNA) are introduced into the bloodstream via the ipsilateral ear vein. The distribution of the radiolabel into various tissues is reported as the per cent of the injected dose per gram of tissue.

The experiment was performed as follows: Aptamer 17.16 and a control RNA of similar length and base composition were transcribed using a 5-fold molar excess of 5'-(O-hexylamino) guanosine monophosphate. Each RNA was conjugated to Hi_{15} at 50 mg/mL aptamer in 30% dimethylformamide with 5 molar equivalents of Hi_{15}-NHS buffered in 100 mM NaBorate pH 9.3, for 30 minutes at room temperature. The conjugation reactions were washed over a 30,000 molecular weight cut-off filter (Microcon 30, Amicon, Inc., Beverly, MA) to remove excess Hi_{15} cage. The RNAs were then labeled with ^{99m}Tc in the following manner: to 1 nmol Hi_{15}-aptamer was added 200 µl of 100 mM $NaPO_4$ buffer, pH 8.5, 23 mg/mL NaTartrate, and 50 µL [^{99m}Tc] pertechnetate (5.0 mCi) eluted from a ^{99}Mo column (Syncor, Denver) within 12 hours prior to use. The labeling reaction was initiated by the addition of 10 µL 5 mg/mL $SnCl_2$. The reaction mixture was incubated for 15 minutes at 90° C. Unreacted ^{99m}Tc was removed by spin dialysis through a 30,000 molecular weight cut-off membrane (Centrex, Schleicher & Schuell) with two 300 µL washes. This labeling protocol results in 30-50% of the added ^{99m}Tc being incorporated with a specific activity of 2-3 mCi/nmol RNA.

For biodistribution studies, rabbits were anesthetized with isofluorane. A two centimeter section of the right jugular vein was isolated *in situ* and all the branches were ligated. A catheter was inserted into the facial vein. The isolated vein segment was temporarily ligated above and below the catheter. The vein segment was flushed with saline. 1000 USP units of heparin was administered intravenously. 300-400 µL of fresh human platelet-rich plasma (citrate) activated with calcium and thrombin was instilled

into the isolated vein segment and allowed to clot. After 30 minutes the ligatures were removed and blood flow over the thrombus was re-established (confirmed by the injection of 200 μl of air into the ipsilateral ear vein). [^{99m}Tc]-conjugated aptamer or control RNA was injected into the ipsilateral ear vein. At 1 hour the rabbit was exsanguinated and tissues were weighed and counted in a Wallac 1470 gamma counter. The aptamer and control RNA were tested at 1 nmol/kg (approximately 0.03 mg/kg).

For aptamer 17.16, radiolabel accumulated in the clot to a significant degree by one hour after injection, while similar accumulation was not observed with the control RNA (FIGURE 6). Blood clearance of the radiolabel was apparently rapid and mediated primarily by a renal mechanism as judged by moderate accumulation of radioactivity in the kidney for both the aptamer and control RNA. Thus, aptamers specific for $\alpha_{IIb}\beta_3$ or for other proteins expressed at high levels on the surface of platelets or within the matrix of a clot will serve as useful agents for rapid imaging of thrombi.

Table 1. αvβ3 Family 1 aptamer sequences.

Clone name (# of isolates)	Sequence of variable region 5'-gggagacaagaauaaacgcucaa [variable region] uucgacaggaggcucacaacaggc-3'	Sequence length	K_D (nM)	SEQ ID NO:
7.3 (2)	uucuacgu uguuuaagggcuuauaugagcgcauuauaccc	40	22	5
7.6; 17.12A	uucaacgc uguuuaagggcuuauaugagcgcguuauaccc	40	ND	6
7.12	uucaacgc uguuuaagggcuuauaugagcgcguuacaccc	40	ND	7
7.24 (5)	uucaacgc uguucaagggcuuauaugagcgcguuauaccc	40	170	8
7.25	uucaacga uguuuaagggcuuauaugagcgcguuauaccc	40	ND	9
7.34	uucau gaa guccaagggcuuauaugagcgcguuauaccc	39	ND	10
7.36 (3)	uucaacgc ugucaaagggcuuauaugagcgcguuauaccc	40	ND	11
7.37 (2)	uu aacgu uguucaaggguuuauaugagugcguuauaccc	39	ND	12
7.38 (2)	uucaacgc uguccaagggcuuauaugagcgcguuauaccc	40	49	13
7.49	uucaacggauguccaagggcuu uaugagcgcguuauaccc	40	ND	14
7.53	uucgacgc uguucaagggcuuauaugagcgcauuauaucc	40	ND	15
7.54 (2)	uucgacgc uguucaagggcuuauaugagcgcguuauaccc	40	230	16
7.57 (2)	uucgacga uguccaagggcuuauaugagcgcauuauaccc	40	ND	17
7.63	uucaacgc uguucaagggcuuauaugagcgcguuacaccc	40	ND	18
7.64	uuc auga uguucaagggcuuauaugagcgcauuauaccc	39	ND	19
7.77 (2)	uucaacga uguugaggggcuuauaugagcgcauuauaccc	40	770	20
7.80	uucaacga uguccaagggcuuauaugagcgcauuauaccc	40	ND	21
7.86	uucaacgc uguucaagggcuuaugugagcgcguuauaccc	40	ND	22
7.91	uucaacgu uguccaagggcuuauaugagcgcauuauaccc	40	ND	23
7.115	uucaacgc uguucaagggcuuauaugagcgcauuauaccc	40	ND	24
7.121	uucaacga uguccaagggcuuauaugagcggauua ccc	38	ND	25
7.124	uucaacac ugu gaagggcuuauaugagcgcgucauaccc	39	ND	26
7.127	uucaacgu uguucaagggcuuauaugagcgcguuauaccc	40	ND	27
15.2	uucaacgu ugucaaagggcuuauaugagcggauua ccc	38	6	28
15.3 (3); 17.17	uucaacgu uguccaagggcuuauaugagcggauua ccc	38	8	29
15.7	uucuacga ugucaaagggcuuauaugagcggauua ccc	38	5	30
15.8	uucgacgc uguugaagggcuuauacgagcggauua ccc	38	5	31
15.10	uucaacgc uguucaagggcuuauaugagcggauua ccc	38	20	32
15.14	uucaacau uguccaagggcuuauaugagcggauua ccc	38	6	33
15.17	uucaacgu ugucaaagggcuuauacgggcggauua ccc	38	4	34
15.18 (2)	uucaacgc ugug aagggcuuauaugagcggauua ccc	37	2	35
15.20	uucaacgc uguccaagggcuuauaugagcgcauuauaccc	40	20	36
15.27	uucgacua uguccaagggcuuauaugagcggauua ccc	38	ND	37
15.28	uucgacga ugucuaagggcuuauaugagcggauua ccc	38	ND	38
15.40; 17.12B	uucaacgc uguugaagggcuuauacgagcggauua ccc	38	ND	39
15.41	uucaacgu uguccaagggcuuauacgagcggauua ccc	38	ND	40
15.42; 17.14 (2)	uucaacgc uguccaagggcuuauacgagcggauua ccc	38	ND	41
15.46; 17.20	uucgacgc ugug aagggcuuauaugagcggauua ccc	37	40	42
15.47	uucaacgu ugucaaagggcuuauacgagcggauua ccc	38	ND	43
15.48	uucaacgc uguugaagggcuuauaugagcggauua ccc	38	ND	44
15.49	uucuacgu ugucuaagggcuuauaugagcggauua ccc	38	ND	45
15.50; 17.3	uucgacgc ugug aagggcuuauacgagcggauua ccc	37	30	46
15.52	uucaacgc uguucaagggcuuauacgagcggauua ccc	38	ND	47
15.53	uucaacgc uguccuagggcuuauaugagcgcaggauaccc	40	70	48
15.55	uucuacgc uguuuaagggcuuauaugagcgaauua ccc	38	ND	49
15.57	uucuacgu uguccaagggcuuauaugagcggauua ccc	38	ND	50
15.58	uucgacgu uguugaagggcuuauaugagcggauua ccc	38	ND	51
17.1	uucaacgc ugucaaagggcuuauauaagcggauua ccc	38	380	52
17.2 (2)	uucuacgc ugug aagggcuuauaugagcggauua ccc	37	2	53
17.5	uucgacgc ugug aagggcuuauaugagcggau acaccc	38	5	54
17.7 (2)	uucuacgc ugug aagggcuuauacgagcggauua ccc	37	6	55
17.8	uucaacgu ugucuaagggcuuauaugagcggauua ccc	38	18	56
17.10	uucuacgu uguugaagggcuuauaugagcggauua ccc	38	ND	57
17.11	uucuacgc ugug aagggcuuauaugagcgaauua ccc	37	4	58
17.13	uucaacgc uguccaagggcuuauaugggcggauua ccc	38	10	59
17.16	uucaacgc ugug aagggcuuauacgagcggauua ccc	37	8	60

Table 2. αvβ3 Family 2 aptamer sequences

Clone name (# of isolates)	Sequence of variable region 5'-gggagacaagaauaaacgcucaa [variable region] uucgacaggaggcucacaacaggc-3'	Sequence length	K_D (nM)	SEQID NO:
7.4	GUACCGGAUCGC**CCUGCC**ACGGUAUUUGAGACAUUGAAA	39	ND	61
7.5 (3)	GGUAGUAAAUGGACU**CCUGCC**AUCCAAUACUAUCUCUGAG	40	>1000	62
7.13	UGUAGUCGCAUGUCGAGCAGCAAUU**CCUGCC**AUUGUAGG	39	>1000	63
7.14 (2)	UGAAGAACUAGA**CCUGCC**CAAGUCCUUCAUCGUGCUUGCU	40	ND	64
7.27 (2)	CGAUUAUACUAUC**CCUGCC**AGUAGUAAUCAGUGCUAUA	38	ND	65
7.29	CGGUGAAGACCUCUAUUAACAACAUGA**CCUGCC**UGCGUUG	40	ND	66
7.32	CGCAAAUAUGUU**CCUGCC**AAAUACGGGCGUUGACGCUAGA	40	ND	67
7.43	GGAC**CCUGCC**GAGCACAUUUAUUCUGGUAACUGAGCCCCC	40	ND	68
7.51	CGCUGAGAGAAAGC**CCUGCC**CUUUCAGCUCGAGAGUUAUA	40	ND	69
7.58	UGAGAUGCAGUU**CCUGCC**UGCUGCAUUUCUUAGAGUGUGU	40	ND	70
7.83	GAUUAACGGUUAU**CCUGCC**AACCGAUUAUAAGAGCAUGGA	40	ND	71
7.89	UGAGAGACUACAAUAGAACUUAUGUAA**CCUGCC**ACAUAGG	40	ND	72
7.97	UAGGAAGUGUAA**CCUGCC**UCACGGUCCUAUCGAGUAGUUU	40	ND	73
7.100	UGAAAACGCAA**CCUGCC**GGCGUCGUCCUUUGGGUAAUUUA	40	ND	74
7.104	AUAGGGGGUUA**CCUGCC**GACCCCAGAAAUAAGCGUGAUU	39	ND	75
7.105	U**CCUGCC**AUAGCGUCUUCAUGUCUGACGUUUGAGUUUCCG	40	ND	76
7.107	UCCUAGGUUGGU**CCUGCC**ACAGCUCAAAGGUUUAGCUUCA	40	ND	77
7.109	ACAUGCAGACAAC**CCUGCC**UUCUGCGUGGUUUAGGAGUA	39	ND	78
7.120	AACCUCAGGCGA**CCUGCC**GCUGUCUGAAGUUCGAGCAUAA	40	ND	79
7.122	ACUCAAGAC**CCUGCC**ACUAUGUGUUACUGAGUAGGAGCGU	40	ND	80
7.125	AUUCGAAAUACGGGUUAAAUC**CCUGCC**UUUAACACGACA	39	ND	81
15.19	UGUAGCCGCAUGUCGAGCAGCAAUU**CCUGCC**AUUGUAGG	39	770	82
15.21	CGGUGAAGACCUCUAUUAACAACAUGA**CCUGCC**UGCGUUG	40	200	83
15.34	UCCCAC**CCUGCC**UUGUCUGUUUGAUAGAGACACUGUCCUU	40	190	84

Table 3. αvβ3 orphan aptamer sequences

Clone name (# of isolates)	Sequence of variable region 5'-gggagacaagaauaaacgcucaa [variable region] uucgacaggaggcucacaacaggc-3'	Sequence length	K_D (nM)	SEQ ID NO:
7.1	gguuugaaagauugccuguagcuccaaaucuuggugagcu	40	ND	85
7.2	ucccgccgauagcuuccacgaagaguuaucuguaaaacaa	40	ND	86
7.11	ugagcuccugauuccaaaccuauuccguuucugggu	36	ND	87
7.30	acuggacaagucaaucucuccggcuugagacuugguuuac	40	ND	88
7.33 (2)	cgagcucuugcuuccaaaccuauuccagacguuu cuggg	40	ND	89
7.41 (2)	gcgagccuauugucuaagaugcaccaggccuguuaagcau	40	>1000	90
7.42	gccuguacggcgauuaugucuuuaccuuaacuguucc	37	ND	91
7.46	uaccaauggcacgaauaacugacuacccccccaaaauggaa	40	ND	92
7.47	gcggggcuuugcucaaguguuugcaaacgguaaauuccac	40	ND	93
7.61	ccuaccgacguccgccgcuggguuaaccuguaaagucacu	40	ND	94
7.66 (2)	gugaaccgauaagcgaaaguaguaccccugcuugacuacu	40	>1000	95
7.67	ggagcuccuaguuccaaaccuauuccagaaguuuucugggu	41	ND	96
7.75	uaguacgcagucauagcggggcagggacuuucuccgugca	40	ND	97
7.76	uuauacugguaugccgccgaccagaauuaauccaaugcgu	40	ND	98
7.82	ugagcuccugguuccaaaccuauuccagacguuucagggu	40	ND	99
7.85	ucuggccugugacuguagucguuucuucgaguugugacgc	40	ND	100
7.92	cucaacgauguccaagggcuuauaugagcgcguuacccc	39	ND	101
7.93	gcgagccuauugucuaagaugcgccaagccuguaaagcau	40	ND	102
7.94	gacuagccggccugagauccuuguucgccacacaugcugg	40	ND	103
7.96	cuucccccgcaaacacauguuuaguacugggagacuuggg	40	ND	104
7.101	ugagcuccugauuccgaaccuauuccagacguuucugggu	40	ND	105
7.102	cugauccucuugucauuguacaucucgcag	30	ND	106
7.106	uacuaagccuaacaaaagagcggauauuggcgcggcacg	39	ND	107
7.108	agucuuaguaguaccgccugcuucuaaccuugggcgcuuu	40	ND	108
7.112	ugauuucaugacuuaugccgccggcaugacuucaaugacg	40	ND	109
7.114	ucaaaggacggaagugccugugcccgacuaaagaguugag	40	ND	110
7.118	cuaucgaucguuuuuucauuuccccccugaccaucgccug	39	ND	111
7.123	uuguccccgcgcagaaacgugacaaauuuaacacgcaccgu	40	ND	112
7.128	uucaacguuguucaagggcuuauaugagcgcguuauaccc	40	ND	113
15.4 (4)	ugauuucaugacuuaugccgccggcaugacuucaaugacg	40	2000	114
15.5	gcauucaaaauuugcgagaacgaauagaaguccgagagcc	40	4000	115
15.13 (2)	gcgggauuuuccugaucaucccacugauucggggccuuac	40	790	116
15.39	ucaaucucggacuagacuaacgaccuugguugacgcuca	39	410	117
15.43	cgccguuaucacgacgugcguucugggcgguacucgcgca	40	45	118